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SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> *Lawsonia intracellularis* subunit vaccines.

<130> 2004.001

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 2088

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (16)..(2085)

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Gly Leu Leu Ser His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile	
15 20 25	

gct aac gta aat aca gta ggc ttt aaa ggc caa cgt atg gat ttc gca	147
Ala Asn Val Asn Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala	
30 35 40	

gac ttt att tat caa gat ggc ttt agt act gca ggg att aca caa att	195
Asp Phe Ile Tyr Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile	
45 50 55 60	

gga cgt ggt gta ggc att gga gct gtc atg ggg aac ttt ggt cag ggt	243
Gly Arg Gly Val Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly	
65 70 75	

agt ttt gaa acc aca act gaa gca aca gac ctt gct att ggt ggt cgt	291
Ser Phe Glu Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg	
80 85 90	

gga ttt ttc aaa gtt aaa cca caa gga tca gag act tca tat tat acc	339
Gly Phe Phe Lys Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr	
95 100 105	

cgt gca ggt aat ttt cgt ttt aat aat gat gga tac tta gtt gat cct	387
Arg Ala Gly Asn Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro	
110 115 120	

cat gga tat gct ctt cag ggt tgg aaa att gat aat act gaa ggg cca	435
His Gly Tyr Ala Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro	
125 130 135 140	

caa cgt atc tca ggt ggt gtt aat cca ggt aca aat act tcg cag att	483
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Gln Arg Ile Ser Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile			
145	150	155	
atg ggt aca ggt gaa cca aca gat atc cgt ctt gat act tgg aca gtt		531	
Met Gly Thr Gly Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val			
160	165	170	
gca cct tta cag aca aca aat gta agt ttt aac gta aac ctt tct tct		579	
Ala Pro Leu Gln Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser			
175	180	185	
gat aaa tct gga gat aaa tct caa aac gtt aat agt cca ttt acc tca		627	
Asp Lys Ser Gly Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser			
190	195	200	
tta ttt aat ata tgg aat ggt aaa caa cca agt gaa cct aac aat cca		675	
Leu Phe Asn Ile Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro			
205	210	215	220
cct atg cct gaa agt gca tat agt tat cag aca tct att aag gta tat		723	
Pro Met Pro Glu Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr			
225	230	235	
gat gaa gct ggt gga aca cat aca tta aca gtc tat ttt gac caa gtt		771	
Asp Glu Ala Gly Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val			
240	245	250	
tct cct aaa gac tac aaa ggt ggt gga agt gga gaa agt gta tgg gaa		819	
Ser Pro Lys Asp Tyr Lys Gly Gly Ser Gly Glu Ser Val Trp Glu			
255	260	265	
tac gtt gtt act atg gat cct tct gaa gat aat cgc caa gtt tct gtt		867	
Tyr Val Val Thr Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val			
270	275	280	
ggg ggt aac att gtg gac atc aaa gat act aaa gct gca gga atg tta		915	
Gly Gly Asn Ile Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu			
285	290	295	300
atg tca gga aca ttg agt ttt gat agc tca gga aaa ctt gca aac caa		963	
Met Ser Gly Thr Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln			
305	310	315	
agt gca tat tcg ctg aat ggt tca cgt aag cct gca gtt gat cct gca		1011	
Ser Ala Tyr Ser Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala			
320	325	330	
acc gga gct ctt att aat ggt aat ggt ttt act att gat aga gat gga		1059	
Thr Gly Ala Leu Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly			
335	340	345	
aat gca att cct att ctt aat ata gat aat cca gct gaa aac ttc tat		1107	
Asn Ala Ile Pro Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr			
350	355	360	
cca gca gaa gtt tct aat aat gga ttt cct atg att gta gct aat ttt		1155	
Pro Ala Glu Val Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe			
365	370	375	380
act ggt gtc cca ggt aaa aat aca gct gga tct gtt ggt gat gct acc		1203	
Thr Gly Val Pro Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr			
385	390	395	
acc ttt ttt aca gaa att gac ttt ggt tta aaa gct act gat ctt gat		1251	
Thr Phe Phe Thr Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp			

400	405	410	
aat aca tgg aag aat gca aat gaa cct ctt tct tct tta agc tat aaa Asn Thr Trp Lys Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys 415	420	425	1299
aaa aca cat aat cct atg gat gtc gca ggt ggt tgg aca gtt ggt ggg Lys Thr His Asn Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly 430	435	440	1347
tat aaa act cca gct cca tca gta act gaa ctt ggt atg gct cag ata Tyr Lys Thr Pro Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile 445	450	455	1395
ttg gaa aat cct gct ggg gta atg cca caa tat tat ttt ggt aac cct Leu Glu Asn Pro Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro 465	470	475	1443
aac tat gat aac aca gtt cca cag agt cca cca tat gta tat aaa aat Asn Tyr Asp Asn Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn 480	485	490	1491
gaa gct tct tat cag gct gca tat aag act gca tta act gcc gca ggt Glu Ala Ser Tyr Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly 495	500	505	1539
ggt acc gca gct gac att aaa aag gaa cat tgg cct cat aat gct gca Gly Thr Ala Ala Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala 510	515	520	1587
tca ggt ata tta gaa gct aat gat cca cca aat gtt aaa gac tta gct Ser Gly Ile Leu Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala 525	530	535	1635
aat atg aat gga aca cca aac cgc tta tca aat gcg ttt act aac tat Asn Met Asn Gly Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr 545	550	555	1683
gca ggt ggt agc tct aca aaa tct gca agt caa aat ggt tat ggt ttt Ala Gly Gly Ser Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe 560	565	570	1731
ggt gat tta atg aac tat agt gta aat gct gag gga gtg tta ttt gga Gly Asp Leu Met Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly 575	580	585	1779
gta tat tca aat gga gta caa ctt cca tta tat caa gta gct ctt tat Val Tyr Ser Asn Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr 590	595	600	1827
gat ttt aac tct aaa cag ggg tta cgt cgt gaa ggt ggt aac tta ttt Asp Phe Asn Ser Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe 605	610	615	1875
agt Caa aca aga gaa tca ggg gac cca tct tca ggt gct gca aac act Ser Gln Thr Arg Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr 625	630	635	1923
tct ggg ttt ggt tca att aac gct aat act tta gaa gga tca aac gta Ser Gly Phe Gly Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val 640	645	650	1971
gat ata tct aca gag ttt gtc tca atg att gca aca caa cgt gga ttc Asp Ile Ser Thr Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe 655	660	665	2019

cag tca aat agt aaa att gta act act att gac caa atg tta gag aca 2067
 Gln Ser Asn Ser Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr
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gtt gta aat atg aag cgt tag 2088
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 685 690

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<213> Lawsonia intracellularis

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 20 25 30

Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala Asp Phe Ile Tyr
 35 40 45

Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile Gly Arg Gly Val
 50 55 60

Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly Ser Phe Glu Thr
 65 70 75 80

Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg Gly Phe Phe Lys
 85 90 95

Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr Arg Ala Gly Asn
 100 105 110

Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro His Gly Tyr Ala
 115 120 125

Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro Gln Arg Ile Ser
 130 135 140

Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly
 145 150 155 160

Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln
 165 170 175

Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly
 180 185 190

Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser Leu Phe Asn Ile
195 200 205

Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro Pro Met Pro Glu
210 215 220

Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr Asp Glu Ala Gly
225 230 235 240

Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val Ser Pro Lys Asp
245 250 255

Tyr Lys Gly Gly Ser Gly Glu Ser Val Trp Glu Tyr Val Val Thr
260 265 270

Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val Gly Gly Asn Ile
275 280 285

Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu Met Ser Gly Thr
290 295 300

Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln Ser Ala Tyr Ser
305 310 315 320

Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala Thr Gly Ala Leu
325 330 335

Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly Asn Ala Ile Pro
340 345 350

Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr Pro Ala Glu Val
355 360 365

Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe Thr Gly Val Pro
370 375 380

Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr Thr Phe Phe Thr
385 390 395 400

Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp Asn Thr Trp Lys
405 410 415

Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys Lys Thr His Asn
420 425 430

Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly Tyr Lys Thr Pro
435 440 445

Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile Leu Glu Asn Pro

450

455

460

Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro Asn Tyr Asp Asn
465 470 475 480

Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn Glu Ala Ser Tyr
485 490 495

Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly Gly Thr Ala Ala
500 505 510

Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala Ser Gly Ile Leu
515 520 525

Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala Asn Met Asn Gly
530 535 540

Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr Ala Gly Gly Ser
545 550 555 560

Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe Gly Asp Leu Met
565 570 575

Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly Val Tyr Ser Asn
580 585 590

Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr Asp Phe Asn Ser
595 600 605

Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe Ser Gln Thr Arg
610 615 620

Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr Ser Gly Phe Gly
625 630 635 640

Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val Asp Ile Ser Thr
645 650 655

Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe Gln Ser Asn Ser
660 665 670

Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr Val Val Asn Met
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Lys Arg
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 Glu Phe Ile Gln Asp Phe Pro Asn Ser Tyr Gln Glu Asp Gly Gln Met
 25 30 35

gtt aca gga att att tca aaa ata ata ggc tct aac tgt gat aat tct 196
 Val Thr Gly Ile Ile Ser Lys Ile Ile Gly Ser Asn Cys Asp Asn Ser
 40 45 50 55

tca aca tct gat ata aat aat aag aaa tcc ata gat aga gat aaa gat	244
Ser Thr Ser Asp Ile Asn Asn Lys Lys Ser Ile Asp Arg Asp Lys Asp	
60 65 70	

aca tta ctc tca agt agt aat aga aat aca ata caa gcc ggt act cca 292
 Thr Leu Leu Ser Ser Asn Arg Asn Thr Ile Gln Ala Gly Thr Pro
 75 80 85

cat caa gaa aat aac ata aaa gaa gat ctt caa ctg act aac aaa aat 340
His Gln Glu Asn Asn Ile Lys Glu Asp Leu Gln Leu Thr Asn Lys Asn
90 95 100 .

gaa caa aca act cca gaa gaa gaa gaa gaa agt aaa ttt att tgg tta 388
 Glu Gln Thr Thr Pro Glu Glu Glu Glu Ser Lys Phe Ile Trp Leu
 105 110 115

aca gaa gct cca tca gag ctt aaa aaa gga gaa aaa gct ata aca caa 436
 Thr Glu Ala Pro Ser Glu Leu Lys Lys Gly Glu Lys Ala Ile Thr Gln
 120 125 130 135

aca aga ttg tct att ggt aag gat ata tct ttt aga att act gct gat 484
 Thr Arg Leu Ser Ile Gly Lys Asp Ile Ser Phe Arg Ile Thr Ala Asp
 140 145 150

gat gcc atc aaa gct caa tca atg atg tta aaa aat cca gat agg ttt 532
Asp Ala Ile Lys Ala Gln Ser Met Met Leu Lys Asn Pro Asp Arg Phe
155 160 165

gtt tta gat ctt caa gga aag tgg ggt att tcc ctt cca cct att cca 580
 Val Leu Asp Leu Gln Gly Lys Trp Gly Ile Ser Leu Pro Pro Ile Pro
 170 175 180

cct aca aat cct tgg tta aaa aaa ata cgc tta ggt act aat aat gga 628
 Pro Thr Asn Pro Trp Leu Lys Lys Ile Arg Leu Gly Thr Asn Asn Gly
 185 190 195

aat aca cga ctt gtc ttt gat ctt caa aaa aaa cca tct aaa act gaa 576
Asn Thr Arg Leu Val Phe Asp Leu Gln Lys Lys Pro Ser Lys Thr Glu
200 205 210 215

att aaa caa tta gat aca aat aaa att gaa atc caa att cattaaattg 725
Ile Lys Gln Leu Asp Thr Asn Lys Ile Glu Ile Gln Ile
220 225

catattagac aataagttat aataaa 751

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Tyr Gln Glu Asp Gly Gln Met Val Thr Gly Ile Ile Ser Lys Ile Ile
35 40 45

Gly Ser Asn Cys Asp Asn Ser Ser Thr Ser Asp Ile Asn Asn Lys Lys
50 55 60

Ser Ile Asp Arg Asp Lys Asp Thr Leu Leu Ser Ser Ser Asn Arg Asn
65 70 75 80

Thr Ile Gln Ala Gly Thr Pro His Gln Glu Asn Asn Ile Lys Glu Asp
85 90 95

Leu Gln Leu Thr Asn Lys Asn Glu Gln Thr Thr Pro Glu Glu Glu Glu
100 105 110

Glu Ser Lys Phe Ile Trp Leu Thr Glu Ala Pro Ser Glu Leu Lys Lys
115 120 125

Gly Glu Lys Ala Ile Thr Gln Thr Arg Leu Ser Ile Gly Lys Asp Ile
130 135 140

Ser Phe Arg Ile Thr Ala Asp Asp Ala Ile Lys Ala Gln Ser Met Met
145 150 155 160

Leu Lys Asn Pro Asp Arg Phe Val Leu Asp Leu Gln Gly Lys Trp Gly
165 170 175

Ile Ser Leu Pro Pro Ile Pro Pro Thr Asn Pro Trp Leu Lys Lys Ile
180 185 190

Arg Leu Gly Thr Asn Asn Gly Asn Thr Arg Leu Val Phe Asp Leu Gln
195 200 205

Lys Lys Pro Ser Lys Thr Glu Ile Lys Gln Leu Asp Thr Asn Lys Ile
210 215 220

Glu Ile Gln Ile
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<213> *Lawsonia intracellularis*

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<222> (34)..(1677)

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gtt gct tta tgt att atg ttt att att atg gtg caa gtt ctt cag gca 102
 Val Ala Leu Cys Ile Met Phe Ile Ile Met Val Gln Val Leu Gln Ala
 10 15 20

aat gca gct agc tat gtg gtt ttg cca ttt aaa gta aat gct cct cca 150
 Asn Ala Ala Ser Tyr Val Val Leu Pro Phe Lys Val Asn Ala Pro Pro
 25 30 35

agc tat act tat ttg gaa aaa gct atc cca tct atg tta act tct aga
 Ser Tyr Thr Tyr Leu Glu Lys Ala Ile Pro Ser Met Leu Thr Ser Arg
 40 45 50 55

ctt tat tgg gaa gaa cgt ttt caa cct atc ccg gat gct aat gct att 246
 Leu Tyr Trp Glu Glu Arg Phe Gln Pro Ile Pro Asp Ala Asn Ala Ile
 60 65 70

aaa gca gga aag gta gaa gat ata aag gaa atg gat aag gca agg ata 294
 Lys Ala Gly Lys Val Glu Asp Ile Lys Glu Met Asp Lys Ala Arg Ile
 75 80 85

gct aca Ggt gca gac tat ctt ata tgg gga cag gta aat att gta ggt 342
 Ala Thr Gly Ala Asp Tyr Leu Ile Trp Gly Gln Val Asn Ile Val Gly
 90 95 100

gat gaa Gct acg ctt gat gta caa gtt tgt gat ata gaa gga tca att 390
 Asp Glu Ala Thr Leu Asp Val Gln Val Cys Asp Ile Glu Gly Ser Ile
 105 110 115

tgg agg aaa agt aaa aat aca aaa gtt gat áat tta att act gcc ctt 438
Trp Arg Lys Ser Lys Asn Thr Lys Val Asp Asn Leu Ile Thr Ala Leu
120 125 130 135

caa gat aca gca gat gca att aat agt gag ttg ttt ggg cgt gca act 486
 Gln Asp Thr Ala Asp Ala Ile Asn Ser Glu Leu Phe Gly Arg Ala Thr
 140 145 150

aca aaa cca tca tca aaa gct act att gta gct caa atg aac tct gga 534
 Thr Lys Pro Ser Ser Lys Ala Thr Ile Val Ala Gln Met Asn Ser Gly
 155 160 165

ttg att aag gga aaa gga aat gaa aat cag tca tat ctt aat cca gaa 582

Leu Ile Lys Gly Lys Gly Asn Glu Asn Gln Ser Tyr Leu Asn Pro Glu			
170	175	180	
ttt cgt tat caa gga agc aat ctt tcc cgt ggc cga agt caa gct ctt		630	
Phe Arg Tyr Gln Gly Ser Asn Leu Ser Arg Gly Arg Ser Gln Ala Leu			
185	190	195	
ccc ttt gct tca gtt ggt ata gtt ggt gac ttt ata gga gat aat		678	
Pro Phe Ala Ser Val Gly Ile Val Val Gly Asp Phe Ile Gly Asp Asn			
200	205	210	215
aaa aat gaa gtt gcc ata tta agt gag tat aaa gtc cat att tat cga		726	
Lys Asn Glu Val Ala Ile Leu Ser Glu Tyr Lys Val His Ile Tyr Arg			
220	225	230	
tgg gaa gaa gaa agg tta gct ctt gga gaa tat aaa ttc cct cgc		774	
Trp Glu Glu Arg Leu Ala Leu Leu Gly Glu Tyr Lys Phe Pro Arg			
235	240	245	
tca cta cag tct tta cat att cgt gct ttt gat gtg gat cat gat ggt		822	
Ser Leu Gln Ser Leu His Ile Arg Ala Phe Asp Val Asp His Asp Gly			
250	255	260	
gta cag gaa atc att gtt tct tgc ttt gat cct tca tat gca aag cca		870	
Val Gln Glu Ile Ile Val Ser Cys Phe Asp Pro Ser Tyr Ala Lys Pro			
265	270	275	
tat tcg ttt att ctt agt ttt aaa aat aga gtg ttt aaa gag tta gcc		918	
Tyr Ser Phe Ile Leu Ser Phe Lys Asn Arg Val Phe Lys Glu Leu Ala			
280	285	290	295
aca aac tta cca ttt tat tta aat gtg gtt aaa ctt cca cca gat ttt		966	
Thr Asn Leu Pro Phe Tyr Leu Asn Val Val Lys Leu Pro Pro Asp Phe			
300	305	310	
tct cct atg tta att ggt caa aag agt gac aat tca agg att ttt tct		1014	
Ser Pro Met Leu Ile Gly Gln Lys Ser Asp Asn Ser Arg Ile Phe Ser			
315	320	325	
ccc tct ggg gtt tat gaa ata gaa aaa cat gga cgt aac tat ata atg		1062	
Pro Ser Gly Val Tyr Glu Ile Glu Lys His Gly Arg Asn Tyr Ile Met			
330	335	340	
gga aat cgt ctt agt ctt cca aag gaa gct aat att ttt aat ttt tct		1110	
Gly Asn Arg Leu Ser Leu Pro Lys Glu Ala Asn Ile Phe Asn Phe Ser			
345	350	355	
tgg tta cca tca gat tca tta aaa gat gaa gaa gct aag tta gta ctt		1158	
Trp Leu Pro Ser Asp Ser Leu Lys Asp Glu Glu Ala Lys Leu Val Leu			
360	365	370	375
gta acc aat aat gaa aga tta gtt gta tat aat aca aaa ggt aca aga		1206	
Val Thr Asn Asn Glu Arg Leu Val Val Tyr Asn Thr Lys Gly Thr Arg			
380	385	390	
ctt ttt atg act gaa gaa gtg tat tat ggt tct tct gtt ggt ata gac		1254	
Leu Phe Met Thr Glu Glu Val Tyr Tyr Gly Ser Ser Val Gly Ile Asp			
395	400	405	
gag ccc agt aat atg cct ggt ctt gga aag tca aaa gag ctt atc cct		1302	
Glu Pro Ser Asn Met Pro Gly Leu Gly Lys Ser Lys Glu Leu Ile Pro			
410	415	420	
tct aaa tat ttt atc cca gga cggt att cct att aat ctt gat tca		1350	
Ser Lys Tyr Phe Ile Pro Gly Arg Met Ile Pro Ile Asn Leu Asp Ser			

425	430	435	
atg ggg aaa tgg gag ttg ctt gta agc aag cca att tct gtt gca gca Met Gly Lys Trp Glu Leu Leu Val Ser Lys Pro Ile Ser Val Ala Ala			1398
440	445	450	455
aaa ttt tt t gaa aat tat aga tct ttt gct gaa ggc gaa att cag gct Lys Phe Phe Glu Asn Tyr Arg Ser Phe Ala Glu Gly Glu Ile Gln Ala			1446
460	465	470	
tta aca tgg gac ggc tta gga tta ggt ctt gta tgg aat aca cgt cgt Leu Thr Trp Asp Gly Leu Gly Leu Gly Leu Val Trp Asn Thr Arg Arg			1494
475	480	485	
att aag gga act att aca gat ttt gcc tta gct gat atg aat aat gat Ile Lys Gly Thr Ile Thr Asp Phe Ala Leu Ala Asp Met Asn Asn Asp			1542
490	495	500	
ggg aag tt a gac tta gtt gtt tcc gtt aat agc cat aca ggg att ctt Gly Lys Leu Asp Leu Val Val Ser Val Asn Ser His Thr Gly Ile Leu			1590
505	510	515	
gga cta gaa aaa cga aag aca att ata gta ttt tat cct tta gag gta Gly Leu Glu Lys Arg Lys Thr Ile Ile Val Phe Tyr Pro Leu Glu Val			1638
520	525	530	535
gat aaa caa ggt atc cct aag gct gtt gaa gat aac taa tttttccta Asp Lys Gln Gly Ile Pro Lys Ala Val Glu Asp Asn			1687
540	545		
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Met Val Gln Val Leu Gln Ala Asn Ala Ala Ser Tyr Val Val Leu Pro			
20	25	30	
Phe Lys Val Asn Ala Pro Pro Ser Tyr Thr Tyr Leu Glu Lys Ala Ile			
35	40	45	
Pro Ser Met Leu Thr Ser Arg Leu Tyr Trp Glu Glu Arg Phe Gln Pro			
50	55	60	
Ile Pro Asp Ala Asn Ala Ile Lys Ala Gly Lys Val Glu Asp Ile Lys			
65	70	75	80
Glu Met Asp Lys Ala Arg Ile Ala Thr Gly Ala Asp Tyr Leu Ile Trp			
85	90	95	
Gly Gln Val Asn Ile Val Gly Asp Glu Ala Thr Leu Asp Val Gln Val			

100

105

110

Cys Asp Ile Glu Gly Ser Ile Trp Arg Lys Ser Lys Asn Thr Lys Val
115 120 125

Asp Asn Leu Ile Thr Ala Leu Gln Asp Thr Ala Asp Ala Ile Asn Ser
130 135 140

Glu Leu Phe Gly Arg Ala Thr Thr Lys Pro Ser Ser Lys Ala Thr Ile
145 150 155 160

Val Ala Gln Met Asn Ser Gly Leu Ile Lys Gly Lys Gly Asn Glu Asn
165 170 175

Gln Ser Tyr Leu Asn Pro Glu Phe Arg Tyr Gln Gly Ser Asn Leu Ser
180 185 190

Arg Gly Arg Ser Gln Ala Leu Pro Phe Ala Ser Val Gly Ile Val Val
195 200 205

Gly Asp Phe Ile Gly Asp Asn Lys Asn Glu Val Ala Ile Leu Ser Glu
210 215 220

Tyr Lys Val His Ile Tyr Arg Trp Glu Glu Glu Arg Leu Ala Leu Leu
225 230 235 240

Gly Glu Tyr Lys Phe Pro Arg Ser Leu Gln Ser Leu His Ile Arg Ala
245 250 255

Phe Asp Val Asp His Asp Gly Val Gln Glu Ile Ile Val Ser Cys Phe
260 265 270

Asp Pro Ser Tyr Ala Lys Pro Tyr Ser Phe Ile Leu Ser Phe Lys Asn
275 280 285

Arg Val Phe Lys Glu Leu Ala Thr Asn Leu Pro Phe Tyr Leu Asn Val
290 295 300

Val Lys Leu Pro Pro Asp Phe Ser Pro Met Leu Ile Gly Gln Lys Ser
305 310 315 320

Asp Asn Ser Arg Ile Phe Ser Pro Ser Gly Val Tyr Glu Ile Glu Lys
325 330 335

His Gly Arg Asn Tyr Ile Met Gly Asn Arg Leu Ser Leu Pro Lys Glu
340 345 350

Ala Asn Ile Phe Asn Phe Ser Trp Leu Pro Ser Asp Ser Leu Lys Asp
355 360 365

Glu Glu Ala Lys Leu Val Leu Val Thr Asn Asn Glu Arg Leu Val Val
370 375 380

Tyr Asn Thr Lys Gly Thr Arg Leu Phe Met Thr Glu Glu Val Tyr Tyr
385 390 395 400

Gly Ser Ser Val Gly Ile Asp Glu Pro Ser Asn Met Pro Gly Leu Gly
405 410 415

Lys Ser Lys Glu Leu Ile Pro Ser Lys Tyr Phe Ile Pro Gly Arg Met
420 425 430

Ile Pro Ile Asn Leu Asp Ser Met Gly Lys Trp Glu Leu Leu Val Ser
435 440 445

Lys Pro Ile Ser Val Ala Ala Lys Phe Phe Glu Asn Tyr Arg Ser Phe
450 455 460

Ala Glu Gly Glu Ile Gln Ala Leu Thr Trp Asp Gly Leu Gly Leu Gly
465 470 475 480

Leu Val Trp Asn Thr Arg Arg Ile Lys Gly Thr Ile Thr Asp Phe Ala
485 490 495

Leu Ala Asp Met Asn Asn Asp Gly Lys Leu Asp Leu Val Val Ser Val
500 505 510

Asn Ser His Thr Gly Ile Leu Gly Leu Glu Lys Arg Lys Thr Ile Ile
515 520 525

Val Phe Tyr Pro Leu Glu Val Asp Lys Gln Gly Ile Pro Lys Ala Val
530 535 540

Glu Asp Asn
545

<210> 7
<211> 1564
<212> DNA
<213> Lawsonia intracellularis

<220>
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<222> (41)..(1522)

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Met Val Ser Tyr Ile
1 5

cgt tta tta gga agt ata ttt tta gta tta gca att ttt ggt tgt ggc Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala Ile Phe Gly Cys Gly	10 15 20	103
gct cag ttt aat aaa ccc tct tta ctt gat gaa acc cct ata gat tac Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu Thr Pro Ile Asp Tyr	25 30 35	151
agt tct gta ctt tct gat tac ata gta gaa tta gaa aaa gaa cca ctt Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu Glu Lys Glu Pro Leu	40 45 50	199
cag tat ata tta cta aaa aaa gaa aaa ttt tct caa atg gag ata tat Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser Gln Met Glu Ile Tyr	55 60 65	247
aat tat caa ttc aca tca caa cat tgg tct cca gat aat ttt gta tca Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro Asp Asn Phe Val Ser	70 75 80 85	295
cct gct ata tgg gaa cat cag gta gat ata tat atc cct cac cat cca Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr Ile Pro His His Pro	90 95 100	343
gtt tca gaa cgt gca ctt ctt atc atc aat aat ggt att aat aat ggt Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn Gly Ile Asn Asn Gly	105 110 115	391
aca ttt ttt act tct cct aaa gct cca act gat ttt act cca gaa gta Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp Phe Thr Pro Glu Val	120 125 130	439
tta gaa gaa atc gct cgt tca aca aaa act gta gtc att gct cta agt Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val Val Ile Ala Leu Ser	135 140 145	487
gat atc cca aat cag tat ctt act tat aga ggt gac tgg aga ttt ctt Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly Asp Trp Arg Phe Leu	150 155 160 165	535
aag gaa gat gaa agt att gct atg agt tgg tct agt ttt tta caa gat Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser Ser Phe Leu Gln Asp	170 175 180	583
cca gaa agt cgg tac aca aga cct ctc tat gtc CCT atg gtt gca gca Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val Pro Met Val Ala Ala	185 190 195	631
gtt tct cag gca atg act ctt gca gaa aag gag tta caa gca tta aaa Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu Leu Gln Ala Leu Lys	200 205 210	679
att aag cat ttt att gta tct ggt gtg tca aag cgt gga tgg aca aca Ile Lys His Phe Ile Val Ser Gly Val Ser Lys Arg Gly Trp Thr Thr	215 220 225	727
tgg ctt tca gct att gct gac tca cga gta gat gct att acc ccg ttt Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp Ala Ile Thr Pro Phe	230 235 240 245	775
gtt att gat gca ttg aat act cgg aaa gtc ctt gga cat atg tat aaa Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu Gly His Met Tyr Lys	250 255 260	823
aca tat gga aat aat tgg cct ata gca ttt tat cca tat tat aga ttt		871

Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr Pro Tyr Tyr Arg Phe
 265 270 275

gat tta gat aaa caa cta gat aca gtt cct ttt ttc aat ctt atg aat 919
 Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe Phe Asn Leu Met Asn
 280 285 290

att gtt gat cca tat aga tat tta gga aca cca tat aag tct cga ctt 967
 Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro Tyr Lys Ser Arg Leu
 295 300 305

gct atc cct aaa tat att gta aat gca agt gga gat gat ttt tat gtc 1015
 Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly Asp Asp Phe Tyr Val
 310 315 320 325

cct gat aat tca agt ttt tac tat gat gat ctc cct gga gag aaa gca 1063
 Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu Pro Gly Glu Lys Ala
 330 335 340

tta cgt ttt gca cca aac tca aat cat cat ggg ata tta aat ttc aca 1111
 Leu Arg Phe Ala Pro Asn Ser Asn His His Gly Ile Leu Asn Phe Thr
 345 350 355

aaa caa tcg ctt att cct ttt gtg aat aga gta caa aaa ggt att tca 1159
 Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val Gln Lys Gly Ile Ser
 360 365 370

acg cca gtt tta gat att tcc aca gag atg acg gaa Cga gtt caa tat 1207
 Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr Glu Arg Val Gln Tyr
 375 380 385

gtg act gtt cgt ttt tct gaa gtt cca gag aag ata gta ctt tgg aaa 1255
 Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys Ile Val Leu Trp Lys
 390 395 400 405

gca gca aat cca gag tca cga gat ttt cgt tat gcc tgc cgt gtt agg 1303
 Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr Ala Cys Arg Val Arg
 410 415 420

tac atg gaa aca cca tta cac ctt tct gca aca ggg gaa gtt agc gtt 1351
 Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr Gly Glu Val Ser Val
 425 430 435

tca tta gag atc cct tct gta gga tgg caa gct gct ttt att gaa gct 1399
 Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala Ala Phe Ile Glu Ala
 440 445 450

aca ttt aaa gat ggt ttt gtt gca aca aca cca gtg tat att tta cca 1447
 Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro Val Tyr Ile Leu Pro
 455 460 465

aaa gat ata tat cca cct ata aaa ata cca cct gta cat gga tta tta 1495
 Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro Val His Gly Leu Leu
 470 475 480 485

tgt aag ttt gta cat ggt cga acc tag taacttagtag ttgttgtact 1542
 Cys Lys Phe Val His Gly Arg Thr
 490

gataatctaa aaggatata at 1564

<210> 8
 <211> 493
 <212> PRT

<213> Lawsonia intracellularis

<400> 8

Met Val Ser Tyr Ile Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala
1 5 10 15

Ile Phe Gly Cys Gly Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu
20 25 30

Thr Pro Ile Asp Tyr Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu
35 40 45

Glu Lys Glu Pro Leu Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser
50 55 60

Gln Met Glu Ile Tyr Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro
65 70 75 80

Asp Asn Phe Val Ser Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr
85 90 95

Ile Pro His His Pro Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn
100 105 110

Gly Ile Asn Asn Gly Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp
115 120 125

Phe Thr Pro Glu Val Leu Glu Ile Ala Arg Ser Thr Lys Thr Val
130 135 140

Val Ile Ala Leu Ser Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly
145 150 155 160

Asp Trp Arg Phe Leu Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser
165 170 175

Ser Phe Leu Gln Asp Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val
180 185 190

Pro Met Val Ala Ala Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu
195 200 205

Leu Gln Ala Leu Lys Ile Lys His Phe Ile Val Ser Gly Val Ser Lys
210 215 220

Arg Gly Trp Thr Thr Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp
225 230 235 240

Ala Ile Thr Pro Phe Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu

245 250 255

Gly His Met Tyr Lys Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr
260 265 270

Pro Tyr Tyr Arg Phe Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe
275 280 285

Phe Asn Leu Met Asn Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro
290 295 300

Tyr Lys Ser Arg Leu Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly
305 310 315 320

Asp Asp Phe Tyr Val Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu
325 330 335

Pro Gly Glu Lys Ala Leu Arg Phe Ala Pro Asn Ser Asn His His Gly
340 345 350

Ile Leu Asn Phe Thr Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val
355 360 365

Gln Lys Gly Ile Ser Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr
370 375 380

Glu Arg Val Gln Tyr Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys
385 390 395 400

Ile Val Leu Trp Lys Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr
405 410 415

Ala Cys Arg Val Arg Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr
420 425 430

Gly Glu Val Ser Val Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala
435 440 445

Ala Phe Ile Glu Ala Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro
450 455 460

Val Tyr Ile Leu Pro Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro
465 470 475 480

Val His Gly Leu Leu Cys Lys Phe Val His Gly Arg Thr
485 490

<212> DNA
<213> *Lawsonia intracellularis*

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<220>
<221> CDS
<222> (12) .. (2096)

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      Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly
      1           5           10

att ggt agt gga acc gat ttc caa gct atg att gat caa ctt aag aaa      98
Ile Gly Ser Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys
      15          20          25

att gag ctt att cct aaa aat aga ctt gta gtt tcc cat gaa caa tgg      146
Ile Glu Leu Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp
      30          35          40          45

aca aaa aaa tat aaa gca ttt gaa gag ctt ata aaa aca gtt aaa gat      194
Thr Lys Lys Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp
      50          55          60

act gaa gcg tct tta agt aag cta agt tct gtt ggt gct att tta aaa      242
Thr Glu Ala Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys
      65          70          75

aaa gaa ggt tct gtt tca aat act tct gtt gca agc gtt aag gca agt      290
Lys Glu Gly Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser
      80          85          90

tct gat gca tct gat gga aca cat aca att gat gtg aaa cag ctt gca      338
Ser Asp Ala Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala
      95          100         105

aca aac acg att ctt tct aat aat cat att ttt gat tct aaa act gaa      386
Thr Asn Thr Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu
      110         115         120         125

agt att aat aat aca ggt tca cct ggt atc ttt gct tat gag tat aaa      434
Ser Ile Asn Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys
      130         135         140

ggg gaa cta cat gaa gtt gaa gtt cct cca ggt agt gat ctt gaa tat      482
Gly Glu Leu His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr
      145         150         155

ctt gca aca tta ata aac aaa gat tct aat aat cct ggt gtt aaa gca      530
Leu Ala Thr Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala
      160         165         170

aac ctt atc aag act ggc gat ggc tat atg ttt agt ctt gaa gga act      578
Asn Leu Ile Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr
      175         180         185

gaa act ggt gca aat gcg act tta tct att tca aat aag aca acg ctt      626
Glu Thr Gly Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu
      190         195         200         205

cca gac ttt aaa gca tct gtt gct acc agc agt gca tta gct aat ggt      674
Pro Asp Phe Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly
      210         215         220

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gaa gat aca att att aat act tca gga aca act caa caa ttt tct ttt Glu Asp Thr Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe 225 230 235	722
gaa tac aat gga aga aca ttt act ttc gat att cct tca gga aca aca Glu Tyr Asn Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr 240 245 250	770
gca aaa gaa ctc caa aca gct ata aat gaa aat aca aaa aat aca gga Ala Lys Glu Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly 255 260 265	818
gta cgt gca act ttt gaa aaa cat ggc tca gat ata gta ttg caa tta Val Arg Ala Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu 270 275 280 285	866
gaa gga aca gtt cct aat caa caa gtt aaa gta acc gct agc cct act Glu Gly Thr Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr 290 295 300	914
gat ctt gga agt ttc aca tct tcg ggt caa gca ggc tgg aat aaa cgt Asp Leu Gly Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg 305 310 315	962
gat tct caa gat gct att ttt aat att aat ggt tgg gac caa gaa ctt Asp Ser Gln Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu 320 325 330	1010
aca tct tct aca aat gaa ctt aca gaa gtt atc cca gga ctt caa att Thr Ser Ser Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile 335 340 345	1058
aca cta ctt tcc gaa ggg aaa aca caa att aca att cag act tct act Thr Leu Leu Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr 350 355 360 365	1106
gac gaa gta aaa aaa caa gtt gag aaa gca gta gag tct ata aat aat Asp Glu Val Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn 370 375 380	1154
gtt ctt tcc aaa att caa gag tta act aaa gca aca gct gaa gac aaa Val Leu Ser Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys 385 390 395	1202
gat gat agt aaa gac act tct agt tct tca agt aaa att cca tca tat Asp Asp Ser Lys Asp Thr Ser Ser Ser Ser Lys Ile Pro Ser Tyr 400 405 410	1250
tta caa agt cct aca aaa gtg aag gct gga cta ttt aca ggt gat act Leu Gln Ser Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr 415 420 425	1298
ggc ata caa atg ctt agt act aga ctt aag tct atc ttt tct tct aat Gly Ile Gln Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn 430 435 440 445	1346
ggt cta ggt ttt tct cct aaa caa aca caa gat ggt cca ggg gat cta Gly Leu Gly Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu 450 455 460	1394
ttt tca tca ctt gct tca att ggt att gtc gta gat gct gat gag ggt Phe Ser Ser Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly 465 470 475	1442
agt gaa act ttt gga caa ctt aaa att tta gat aga gaa aca att ggt	1490

Ser Glu Thr Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly
 480 485 490

cct gat gca cct tat aca act ctt gat gag gca tta aaa aaa gat cca 1538
 Pro Asp Ala Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro
 495 500 505

caa gca gta gca gat ata tta gct ggt agt tct gga ata tct gat tca 1586
 Gln Ala Val Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser
 510 515 520 525

aca gat ttt tct tat caa gat cat att gtt gga aaa aca caa gct ggt 1634
 Thr Asp Phe Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly
 530 535 540

aca tat gat gta aag tat tct gta gat gca agt ggt act ata gga gac 1682
 Thr Tyr Asp Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp
 545 550 555

gtt tac att gga ggt gta aaa gct tct cta tct gat cct gca aaa aat 1730
 Val Tyr Ile Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn
 560 565 570

ata tat acg gtc aca tct ggt cct gct aca ggt ctt agt ata gca gtt 1778
 Ile Tyr Thr Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val
 575 580 585

aat aat cgt act cca ggt atc aat gta gaa agt act gta aga gtc aaa 1826
 Asn Asn Arg Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys
 590 595 600 605

caa ggt aaa ctt agc caa ata caa gaa gca ctt aaa gct gaa gta cag 1874
 Gln Gly Lys Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln
 610 615 620

caa gat cct tta aaa gaa aac aca ggt cct tta att atc atg caa gat 1922
 Gln Asp Pro Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp
 625 630 635

aac tat aag gat gtt atg aaa aat ctt gag aca aga ata gaa aaa gaa 1970
 Asn Tyr Lys Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu
 640 645 650

aca caa aga gtt act agt tgg gaa cgt atg atg cgt tta aaa ttt tct 2018
 Thr Gln Arg Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser
 655 660 665

aga ctt gat gct gta tta gca aaa tat aat cag atg atg tca gca aat 2066
 Arg Leu Asp Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn
 670 675 680 685

gct tct agt tta ggg caa ctt ggt gca taa
 Ala Ser Ser Leu Gly Gln Leu Gly Ala
 690

<210> 10
 <211> 694
 <212> PRT
 <213> Lawsonia intracellularis

<400> 10

Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly Ile Gly Ser
 1 5 10 15

Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys Ile Glu Leu
20 25 30

Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp Thr Lys Lys
35 40 45

Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp Thr Glu Ala
50 55 60

Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys Lys Glu Gly
65 70 75 80

Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser Ser Asp Ala
85 90 95

Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala Thr Asn Thr
100 105 110

Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu Ser Ile Asn
115 120 125

Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys Gly Glu Leu
130 135 140

His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr Leu Ala Thr
145 150 155 160

Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala Asn Leu Ile
165 170 175

Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr Glu Thr Gly
180 185 190

Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu Pro Asp Phe
195 200 205

Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly Glu Asp Thr
210 215 220

Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe Glu Tyr Asn
225 230 235 240

Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr Ala Lys Glu
245 250 255

Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly Val Arg Ala
260 265 270

Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu Glu Gly Thr
275 280 285

Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr Asp Leu Gly
290 295 300

Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg Asp Ser Gln
305 310 315 320

Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu Thr Ser Ser
325 330 335

Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile Thr Leu Leu
340 345 350

Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr Asp Glu Val
355 360 365

Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn Val Leu Ser
370 375 380

Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys Asp Asp Ser
385 390 395 400

Lys Asp Thr Ser Ser Ser Ser Lys Ile Pro Ser Tyr Leu Gln Ser
405 410 415

Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr Gly Ile Gln
420 425 430

Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn Gly Leu Gly
435 440 445

Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu Phe Ser Ser
450 455 460

Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly Ser Glu Thr
465 470 475 480

Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly Pro Asp Ala
485 490 495

Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro Gln Ala Val
500 505 510

Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser Thr Asp Phe
515 520 525

Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly Thr Tyr Asp
 530 535 540

Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp Val Tyr Ile
 545 550 555 560

Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn Ile Tyr Thr
 565 570 575

Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val Asn Asn Arg
 580 585 590

Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys Gln Gly Lys
 595 600 605

Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln Gln Asp Pro
 610 615 620

Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp Asn Tyr Lys
 625 630 635 640

Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu Thr Gln Arg
 645 650 655

Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser Arg Leu Asp
 660 665 670

Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn Ala Ser Ser
 675 680 685

Leu Gly Gln Leu Gly Ala
 690

<210> 11
 <211> 1200
 <212> DNA
 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (13)..(1200)

<400> 11
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 Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu
 1 5 10

tcc aca aca aat caa atg acc aat gca gct gct ggt aat act aat aga 99
 Ser Thr Thr Asn Gln Met Thr Asn Ala Ala Gly Asn Thr Asn Arg
 15 20 25

gct acc ggt agt atg aac ggt cgt aat ctc aca caa ata aaa aca cct 147
 Ala Thr Gly Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro

30	35	40	45	
cag tcc atg att gat aat gct tca gaa gaa tta aca act tct ctt				gaa 195
Gln Ser Met Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu				Glu
50	55		60	
tct aaa agc agt gac gac ttt gca att aaa gat cgt aaa aga caa				ggg 243
Ser Lys Ser Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln				Gly
65	70		75	
aaa gga tct gat tct cta tta aaa atg gtt caa gaa tat aca gag				ctg 291
Lys Gly Ser Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu				Leu
80	85		90	
acg aat gat gat acc cgt aat gct aaa aga gct atg tta tcc cag				gta 339
Thr Asn Asp Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln				Val
95	100		105	
tta cgt gca agt caa agt tca caa gat gta ctc gaa aaa aca tta				gaa 387
Leu Arg Ala Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu				Glu
110	115		120	125
caa ttt tct aat aaa aca gat gct tgg gct tct ctt gca gaa att				gca 435
Gln Phe Ser Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile				Ala
130	135		140	
caa gaa tat ggt gca gaa tct cca cag cca aca gga tta aaa tct				gta 483
Gln Glu Tyr Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser				Val
145	150		155	
tta gat gct atg gag aca tta gaa aat gag ttt ggt gat gaa att				aaa 531
Leu Asp Ala Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile				Lys
160	165		170	
gca gga cta aaa gga gct cta aat tca aaa gaa ttt act gat ata				ggc 579
Ala Gly Leu Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile				Gly
175	180		185	
agt gca gca cag tta aga gat ctt tat aca aca aca gta act ata				aca 627
Ser Ala Ala Gln Leu Arg Asp Leu Tyr Thr Thr Val Thr Ile				Thr
190	195		200	205
gct gca cct gat gca gtg tta gca aga ctt ctt gaa gaa tat gag				agt 675
Ala Ala Pro Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr				Ser
210	215		220	
gat gat gat ctg gat aga gcc att gat ttc ctt cta tct aca ctt				ggt 723
Asp Asp Asp Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr				Leu Gly
225	230		235	
gga gag ctt gaa tca gct gat cca agt atg gat aaa gta cat ctt				Caa 771
Gly Glu Leu Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu				Gln
240	245		250	
agt gta atg ggt gat att gaa aaa aca caa ctt cat agc tct				Cat 819
Ser Val Met Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser				Ser His
255	260		265	
aaa caa tgt act aca gcc ctt agc agg tgg aaa gag aaa cat aaa				ggt 867
Lys Gln Cys Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys				Gly
270	275		280	285
ggg ggg gaa aat agt aca cta act cct tta gaa atg atg cgt gaa				c ta 915
Gly Gly Glu Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg				Glu Leu
290	295		300	

att gca cta aaa aat gaa aat ttt att tct cct tcc tct ata gat aaa Ile Ala Leu Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys 305 310 315	963
att gtt gat caa gct gat ccc caa gat att gaa aaa gaa gtc ctt ttt Ile Val Asp Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe 320 325 330	1011
tta caa gag atg tta gct gct gta aga aaa ttt ccc att atg gta ttt Leu Gln Glu Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe 335 340 345	1059
gat aat gtc gaa aat cgt gta aga gtt atg ggt gct gta caa gat gct Asp Asn Val Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala 350 355 360 365	1107
gtt gac gat gct gta aga aga gaa gat gaa ttc ctc ttt caa aaa gaa Val Asp Asp Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu 370 375 380	1155
cat cct gat gta cca cta caa cca gat gaa aat aat ata caa taa His Pro Asp Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln 385 390 395	1200
<210> 12 <211> 395 <212> PRT <213> Lawsonia intracellularis	
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Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu Ser Thr Thr 1 5 10 15	
Asn Gln Met Thr Asn Ala Ala Gly Asn Thr Asn Arg Ala Thr Gly 20 25 30	
Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro Gln Ser Met 35 40 45	
Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu Ser Lys Ser 50 55 60	
Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly Lys Gly Ser 65 70 75 80	
Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu Thr Asn Asp 85 90 95	
Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val Leu Arg Ala 100 105 110	
Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu Gln Phe Ser 115 120 125	

Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala Gln Glu Tyr
130 135 140

Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val Leu Asp Ala
145 150 155 160

Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys Ala Gly Leu
165 170 175

Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly Ser Ala Ala
180 185 190

Gln Leu Arg Asp Leu Tyr Thr Thr Val Thr Ile Thr Ala Ala Pro
195 200 205

Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser Asp Asp Asp
210 215 220

Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly Gly Glu Leu
225 230 235 240

Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln Ser Val Met
245 250 255

Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His Lys Gln Cys
260 265 270

Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly Gly Glu
275 280 285

Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu Ile Ala Leu
290 295 300

Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys Ile Val Asp
305 310 315 320

Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe Leu Gln Glu
325 330 335

Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe Asp Asn Val
340 345 350

Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala Val Asp Asp
355 360 365

Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu His Pro Asp
370 375 380

Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln

385	390	395	
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<211> 1269			
<212> DNA			
<213> Lawsonia intracellularis			
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<222> (32)..(1222)			
<400> 13			
tgttggaaat tctctctgga ggagtaaaagc a atg aca aat ttt gga gat ata			52
Met Thr Asn Phe Gly Asp Ile			
1		5	
agc gga agc tcc gca aga atg agt agc ttg atg act ggt aca tcc ggt			100
Ser Gly Ser Ser Ala Arg Met Ser Ser Leu Met Thr Gly Thr Ser Gly			
10	15	20	
gaa gaa gga ctt gaa gaa ctt gaa ggt ggt gtt cct aaa gag caa ggt			148
Glu Glu Gly Leu Glu Glu Leu Glu Gly Gly Val Pro Lys Glu Gln Gly			
25	30	35	
ggt cca ggt aaa gga gat gct tca gag gct gct aaa ggt caa gca gca			196
Gly Pro Gly Lys Gly Asp Ala Ser Glu Ala Ala Lys Gly Gln Ala Ala			
40	45	50	55
gca gat agt att aat tca gct ggt act gaa aag cct gga gaa gtt			244
Ala Asp Ser Ile Asn Ser Ala Gly Gly Thr Glu Lys Pro Gly Glu Val			
60	65	70	
ggt gat aag gaa gat gta ggg gaa ggt ggc gaa ata cct gaa ggt ggt			292
Gly Asp Lys Glu Asp Val Gly Glu Gly Glu Ile Pro Glu Gly Gly			
75	80	85	
gaa ata cct gag ggt ggt gaa gaa gtt cca gag gaa ccc cca tat gtc			340
Glu Ile Pro Glu Gly Gly Glu Val Pro Glu Glu Pro Pro Tyr Val			
90	95	100	
cct cct cca ttg gtt gaa cca gct aaa atc agt aca gta aca gat ctc			388
Pro Pro Pro Leu Val Glu Pro Ala Lys Ile Ser Thr Val Thr Asp Leu			
105	110	115	
agt acg tta atg gga tca cta cag ctg aca gag caa aaa aag aat gct			436
Ser Thr Leu Met Gly Ser Leu Gln Leu Thr Glu Gln Lys Lys Asn Ala			
120	125	130	135
gaa aaa aca gta aat gaa att aaa gca cag aat aaa gag caa caa gta			484
Glu Lys Thr Val Asn Glu Ile Lys Ala Gln Asn Lys Glu Gln Gln Val			
140	145	150	
aag ttc caa gag caa att aaa aag att gag gat aat att gct gaa tct			532
Lys Phe Gln Glu Gln Ile Lys Ile Glu Asp Asn Ile Ala Glu Ser			
155	160	165	
aag aaa agt ggt ata ctt aag ttt ttc caa aag ttg ttt gca gtt att			580
Lys Lys Ser Gly Ile Leu Lys Phe Phe Gln Lys Leu Phe Ala Val Ile			
170	175	180	
ggt gct gta cta gga gct att gga ggt gcg cta gct att gct gca ggt			628
Gly Ala Val Leu Gly Ala Ile Gly Gly Ala Leu Ala Ile Ala Ala Gly			
185	190	195	

gct gct tca ggt aac cca tta ttg gtt gct gca ggt att atg gct att Ala Ala Ser Gly Asn Pro Leu Leu Val Ala Ala Gly Ile Met Ala Ile 200 205 210 215	676
gta gct tca att gat gca gca atg tcg tcg cta tcg gat ggt aaa gtg Val Ala Ser Ile Asp Ala Ala Met Ser Ser Leu Ser Asp Gly Lys Val 220 225 230	724
tcc atc tca gca ggg att agt aag gct ct t gag gct atg gga gta cca Ser Ile Ser Ala Gly Ile Ser Lys Ala Leu Glu Ala Met Gly Val Pro 235 240 245	772
gca gaa aca gca caa tgg att gca ttt ggt ata cag tta gca atg att Ala Glu Thr Ala Gln Trp Ile Ala Phe Gly Ile Gln Leu Ala Met Ile 250 255 260	820
gca gtg act ata gct att ggt ttt gcc tc t ggt ggt gga gca atg Ala Val Thr Ile Ala Ile Gly Phe Ala Ser Gly Gly Gly Ala Met 265 270 275	868
gct gga gtg tca aaa ata gca gat atg ttt tca aag tct caa gat gta Ala Gly Val Ser Lys Ile Ala Asp Met Phe Ser Lys Ser Gln Asp Val 280 285 290 295	916
gct aag ttg gca cag att gaa aaa gct tct aaa ata gta caa atc Ala Lys Leu Ala Gln Met Ile Glu Lys Ala Ser Lys Ile Val Gln Ile 300 305 310	964
gct ggt tca gtt aat cag tct gct ata gg C ggt aca ggt att ggt aca Ala Gly Ser Val Asn Gln Ser Ala Ile Gly Gly Thr Gly Ile Gly Thr 315 320 325	1012
gct gta gtg caa agc aat ata aaa gct aat gaa tct gaa caa aaa gaa Ala Val Val Gln Ser Asn Ile Lys Ala Asn Glu Ser Glu Gln Lys Glu 330 335 340	1060
att gaa gct gct att gca aaa gtt aaa gct aag ata gag acg tta caa Ile Glu Ala Ala Ile Ala Lys Val Lys Ala Lys Ile Glu Thr Leu Gln 345 350 355	1108
gac ttc ttt aaa aac caa atg gaa caa ttc aat gct ata atg aaa ata Asp Phe Phe Lys Asn Gln Met Glu Gln Phe Asn Ala Ile Met Lys Ile 360 365 370 375	1156
ata aca gat att att caa gat agc gtc aat aca aaa ata gct gtt caa Ile Thr Asp Ile Ile Gln Asp Ser Val Asn Thr Lys Ile Ala Val Gln 380 385 390	1204
cgt ggt gca cgt gag taa taccttagt aaat acagtg actataactat Arg Gly Ala Arg Glu 395	1252
aatatataaa ttaataaa	1269

<210> 14
 <211> 396
 <212> PRT
 <213> Lawsonia intracellularis
 <400> 14

Met Thr Asn Phe Gly Asp Ile Ser Gly Ser Ser Ala Arg Met Ser Ser
 1 5 10 15

Leu Met Thr Gly Thr Ser Gly Glu Glu Gly Leu Glu Glu Leu Glu Gly
20 25 30

Gly Val Pro Lys Glu Gln Gly Gly Pro Gly Lys Gly Asp Ala Ser Glu
35 40 45

Ala Ala Lys Gly Gln Ala Ala Ala Asp Ser Ile Asn Ser Ala Gly Gly
50 55 60

Thr Glu Lys Pro Gly Glu Val Gly Asp Lys Glu Asp Val Gly Glu Gly
65 70 75 80

Gly Glu Ile Pro Glu Gly Gly Glu Ile Pro Glu Gly Gly Glu Glu Val
85 90 95

Pro Glu Glu Pro Pro Tyr Val Pro Pro Pro Leu Val Glu Pro Ala Lys
100 105 110

Ile Ser Thr Val Thr Asp Leu Ser Thr Leu Met Gly Ser Leu Gln Leu
115 120 125

Thr Glu Gln Lys Lys Asn Ala Glu Lys Thr Val Asn Glu Ile Lys Ala
130 135 140

Gln Asn Lys Glu Gln Gln Val Lys Phe Gln Glu Gln Ile Lys Lys Ile
145 150 155 160

Glu Asp Asn Ile Ala Glu Ser Lys Ser Gly Ile Leu Lys Phe Phe
165 170 175

Gln Lys Leu Phe Ala Val Ile Gly Ala Val Leu Gly Ala Ile Gly Gly
180 185 190

Ala Leu Ala Ile Ala Ala Gly Ala Ala Ser Gly Asn Pro Leu Leu Val
195 200 205

Ala Ala Gly Ile Met Ala Ile Val Ala Ser Ile Asp Ala Ala Met Ser
210 215 220

Ser Leu Ser Asp Gly Lys Val Ser Ile Ser Ala Gly Ile Ser Lys Ala
225 230 235 240

Leu Glu Ala Met Gly Val Pro Ala Glu Thr Ala Gln Trp Ile Ala Phe
245 250 255

Gly Ile Gln Leu Ala Met Ile Ala Val Thr Ile Ala Ile Gly Phe Ala
260 265 270

Ser Gly Gly Gly Ala Met Ala Gly Val Ser Lys Ile Ala Asp Met
 275 280 285

Phe Ser Lys Ser Gln Asp Val Ala Lys Leu Ala Gln Met Ile Glu Lys
 290 295 300

Ala Ser Lys Ile Val Gln Ile Ala Gly Ser Val Asn Gln Ser Ala Ile
 305 310 315 320

Gly Gly Thr Gly Ile Gly Thr Ala Val Val Gln Ser Asn Ile Lys Ala
 325 330 335

Asn Glu Ser Glu Gln Lys Glu Ile Glu Ala Ala Ile Ala Lys Val Lys
 340 345 350

Ala Lys Ile Glu Thr Leu Gln Asp Phe Phe Lys Asn Gln Met Glu Gln
 355 360 365

Phe Asn Ala Ile Met Lys Ile Ile Thr Asp Ile Ile Gln Asp Ser Val
 370 375 380

Asn Thr Lys Ile Ala Val Gln Arg Gly Ala Arg Glu
 385 390 395

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<211> 894
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (13)..(894)

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Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn
1 5 10

gct caa cgt aac tta agc aag tct tat gga gaa ctg agt tct tct gtt 99
Ala Gln Arg Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val
15 20 25

cga aaa ctt tct tca ggt ctt cgt gta gga act gct gct gat gac tca 147
Arg Lys Leu Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser
30 35 40 45

gca ggg tta gcc att cga gaa ctc atg aga tct gac att gca aca aca 195
Ala Gly Leu Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr
50 55 60

caa caa gga ata cga aat gcg aat gat gct att tct atg att caa act 243
Gln Gln Gly Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr
65 70 75

gcg gat ggt gca ctt gga gtc atc gat gaa aag ctc att cga atg aaa 291

Ala Asp Gly Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys		
80	85	90
gaa ctt gct gaa caa qct gct aca ggt aca tat aac tcc act cag cgt		339
Glu Leu Ala Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg		
95	100	105
atg att att gac tct gaa tat caa gct atg gcc tca gaa att act cgt		387
Met Ile Ile Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg		
110	115	120
att gct aat gcg aca gaa ttt aat ggt ata aaa ctt ctt gat ggt tca		435
Ile Ala Asn Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser		
130	135	140
tta tca ggt aat cat gat ggg aaa aaa ata aat tca act ggt gca gta		483
Leu Ser Gly Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val		
145	150	155
cgt atc cac ttt ggg aca tct aac agc tct gct gaa gat tac tat gat		531
Arg Ile His Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp		
160	165	170
att aaa att ggt ggc tct aca gct tct gca tta gga ctt ggt aat aca		579
Ile Lys Ile Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr		
175	180	185
gta aaa ggt gcg ggt gct aca gtc tct act caa gct gca gca caa aat		627
Val Lys Gly Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn		
190	195	200
205		
gcc tta aaa gct ata gat aat gcc att gtt tca aaa gat aaa att cga		675
Ala Leu Lys Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg		
210	215	220
gca cac ctt ggt gga tta caa aat aga ctt gaa gct aca gtt gat aat		723
Ala His Leu Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn		
225	230	235
tta agt ata caa aat gaa aac tta caa gct gct gaa tct cgt ata tct		771
Leu Ser Ile Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser		
240	245	250
gat ata gat gta agc caa gaa atg aca caa ttt gta cgt aac caa ata		819
Asp Ile Asp Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile		
255	260	265
ctt aca caa aca ggt gtt gct atg ctt tca caa gct aat tct cta cca		867
Leu Thr Gln Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro		
270	275	280
285		
cgt atg gct cag caa ctt att ggc taa		894
Arg Met Ala Gln Gln Leu Ile Gly		
290		

<210> 16
<211> 293
<212> PRT
<213> Lawsonia intracellularis

<400> 16

Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn Ala Gln Arg
1 5 10 15

Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val Arg Lys Leu
20 25 30

Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser Ala Gly Leu
35 40 45

Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr Gln Gln Gly
50 55 60

Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr Ala Asp Gly
65 70 75 80

Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys Glu Leu Ala
85 90 95

Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg Met Ile Ile
100 105 110

Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg Ile Ala Asn
115 120 125

Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser Leu Ser Gly
130 135 140

Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val Arg Ile His
145 150 155 160

Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp Ile Lys Ile
165 170 175

Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr Val Lys Gly
180 185 190

Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn Ala Leu Lys
195 200 205

Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg Ala His Leu
210 215 220

Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn Leu Ser Ile
225 230 235 240

Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser Asp Ile Asp
245 250 255

Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile Leu Thr Gln
260 265 270

Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro Arg Met Ala
275 280 285

Gln Gln Leu Ile Gly
29 O

<210> 17
<211> 2848
<212> DNA
<213> *Lawsonia intracellularis*

<220>
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<222> (29)..(2848)

<400> 17
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Met Tyr Asn Ile Ile Asn Lys His
1 5

caa atc ata aaa att tta tta ttt tcc tta tgt gtt ttc ttt ttt aca 100
 Gln Ile Ile Lys Ile Leu Leu Phe Ser Leu Cys Val Phe Phe Phe Thr
 10 15 20

ctt aca gaa aaa caa aaa att tat gct gca gac gtc ttt ttt gag ggc 148
 Leu Thr Glu Lys Gln Lys Ile Tyr Ala Ala Asp Val Phe Phe Glu Gly
 25 30 35 40

aga acc gaa acc tta atc aat gta aac aaa cca ttt gat tct ttt ttt 196
 Arg Thr Glu Thr Leu Ile Asn Val Asn Lys Pro Phe Asp Ser Phe Phe
 45 50 55

gga ggt tct gac tct aca ata gga acc ctt gaa aca gga cct act aat 244
 Gly Gly Ser Asp Ser Thr Ile Gly Thr Leu Glu Thr Gly Pro Thr Asn
 60 65 70

ctt acc ttc aca aca gta gga gcc ttc cgc aat tct gtt ttc aga att 292
 Leu Thr Phe Thr Thr Val Gly Ala Phe Arg Asn Ser Val Phe Arg Ile
 75 80 85

att ggt ggt ggt agg tct agt ttt aac aac cca	aat aca gtt aaa ggc	340
Ile Gly Gly Gly Arg Ser Ser Phe Asn Asn Pro	Asn Thr Val Lys Gly	
90	95	100

aat gtt act cta act gtt tat aat act gat gta gaa aga ata att ggt 388
 Asn Val Thr Leu Thr Val Tyr Asn Thr Asp Val Glu Arg Ile Ile Gly
 105 110 115 120

gca ggt atc agc aat aga gga ctt gta acc gtt act ggc tca gta aat 436
Ala Gly Ile Ser Asn Arg Gly Leu Val Thr Val Thr Gly Ser Val Asn
125 130 135

atg aag cta gaa aat gtt tct gtt act aga gga att tat ggt ggt gtc 484
Met Lys Leu Glu Asn Val Ser Val Thr Arg Gly Ile Tyr Gly Gly Val
140 145 150

tat act caa aat gga cat gta cta ggc tct atc aac atg cat ttg aaa 532
 Tyr Thr Gln Asn Gly His Val Leu Gly Ser Ile Asn Met His Leu Lys
 155 160 165

aac gtc caa act cca cta tta ata ggt tct gga gta agc aat gga cct 580

Asn Val Gln Thr Pro Leu Leu Ile Gly Ser Gly Val Ser Asn Gly Pro			
170	175	180	
aat cgt att act gta aat gga gac ata aac att gat gtt gaa gac tct			628
Asn Arg Ile Thr Val Asn Gly Asp Ile Asn Ile Asp Val Glu Asp Ser			
185	190	195	200
agg att caa tat gta aac att aca gga gaa gta gat gca ggg ata aaa			676
Arg Ile Gln Tyr Val Asn Ile Thr Gly Glu Val Asp Ala Gly Ile Lys			
205	210	215	
gga aat gct act cta act gta aaa aaa tct act gtt gag ctt ata aac			724
Gly Asn Ala Thr Leu Thr Val Lys Lys Ser Thr Val Glu Leu Ile Asn			
220	225	230	
tct ggt aga ggt aat atc tta ggt aat ctc aaa ata tct ata gca gat			772
Ser Gly Arg Gly Asn Ile Leu Gly Asn Leu Lys Ile Ser Ile Ala Asp			
235	240	245	
tca aat ata agg ggg tta tca cca gta gac ttt ggt tct tca gta tat			820
Ser Asn Ile Arg Gly Leu Ser Pro Val Asp Phe Gly Ser Ser Val Tyr			
250	255	260	
ggg gac aca tct ata aat gta att aat tct cag att aat gat att act			868
Gly Asp Thr Ser Ile Asn Val Ile Asn Ser Gln Ile Asn Asp Ile Thr			
265	270	275	280
ctt ata cca agg gct ggt gga atg ctt gta ggt cct gtt acc cta gat			916
Leu Ile Pro Arg Ala Gly Gly Met Leu Val Gly Pro Val Thr Leu Asp			
285	290	295	
atc aca agc agt act ata caa aat ata caa tgt ggg cct gtc agt caa			964
Ile Thr Ser Ser Thr Ile Gln Asn Ile Gln Cys Gly Pro Val Ser Gln			
300	305	310	
aat aat caa ctt aac aca cta aat gta act gtt aat act agt aac att			1012
Asn Asn Gln Leu Asn Thr Leu Asn Val Thr Val Asn Thr Ser Asn Ile			
315	320	..	325
act aac tta aac ctt ggt agt gtc gaa ggt cat aca ata tca act aca			1060
Thr Asn Leu Asn Leu Gly Ser Val Glu Gly His Thr Ile Ser Thr Thr			
330	335	340	
gca act gtt act gat aat att act aac ctt aat gtc gga acc ttc			1108
Ala Thr Val Thr Asp Ser Asn Ile Thr Asn Leu Asn Val Gly Thr Phe			
345	350	355	360
aat gga ctt gga gta act gag aat gcc tct gta atc att aat agt ggc			1156
Asn Gly Leu Gly Val Thr Glu Asn Ala Ser Val Ile Ile Asn Ser Gly			
365	370	375	
aat att act aac ctt aat gtc gga act aat gta ata gct gca gcc aca			1204
Asn Ile Thr Asn Leu Asn Val Gly Thr Asn Val Ile Ala Ala Thr			
380	385	390	
act att aat tcc tct gcg acc ata cac gac gga ctt att gca aac ctt			1252
Thr Ile Asn Ser Ser Ala Thr Ile His Asp Gly Leu Ile Ala Asn Leu			
395	400	405	
acc tta ggc tca caa ggt aat ggt cgt act atg ata gct aca gca aat			1300
Thr Leu Gly Ser Gln Gly Asn Gly Arg Thr Met Ile Ala Thr Ala Asn			
410	415	420	
gtt aat ggt gga act att gga tta tta act atg ggt tca gaa aac ttc			1348
Val Asn Gly Gly Thr Ile Gly Leu Leu Thr Met Gly Ser Glu Asn Phe			

425	430	435	440	
ata cca ggc aca aga cca att act gaa tta gca ata cta aac atg tct Ile Pro Gly Thr Arg Pro Ile Thr Glu Leu Ala Ile Leu Asn Met Ser				1396
445	450	455		
ggt gga tta att gaa aga att atc gta ggt aat gcc aac tct tca acc Gly Gly Leu Ile Glu Arg Ile Ile Val Gly Asn Ala Asn Ser Ser Thr				1444
460	465	470		
ata aac ttt act cct ggg aag aga tca att gta aaa aca ata aat ggt Ile Asn Phe Thr Pro Gly Lys Arg Ser Ile Val Lys Thr Ile Asn Gly				1492
475	480	485		
cca gaa ctt cca tat tta gtt aac ata caa aaa ggt gct atg aca caa Pro Glu Leu Pro Tyr Leu Val Asn Ile Gln Lys Gly Ala Met Thr Gln				1540
490	495	500		
tgg ggc act aaa aat atg ccc ttt tta ttg gat aca aga aat tta atc Trp Gly Thr Lys Asn Met Pro Phe Leu Leu Asp Thr Arg Asn Leu Ile				1588
505	510	515	520	
ttg tcc gga act ctg att acc tca aat att caa cta gct gat tta tct Leu Ser Gly Thr Leu Ile Thr Ser Asn Ile Gln Leu Ala Asp Leu Ser				1636
525	530	535		
ata acc aat cta ttt gtt gct aat ggc ggt aca cta gta cct aga aaa Ile Thr Asn Leu Phe Val Ala Asn Gly Gly Thr Leu Val Pro Arg Lys				1684
540	545	550		
tta ata cct ggg aac caa cct gtt ata cag ttt ctt gga ggt cct caa Leu Ile Pro Gly Asn Gln Pro Val Ile Gln Phe Leu Gly Gly Pro Gln				1732
555	560	565		
tca ctc tta gtt atc cat caa cca tta aaa gta aat tta agc tta tca Ser Leu Leu Val Ile His Gln Pro Leu Lys Val Asn Leu Ser Leu Ser				1780
570	575	580		
cca aaa ctt att gga agt agc atg gtg cca ctt gct ttt gtc tct caa Pro Lys Leu Ile Gly Ser Ser Met Val Pro Leu Ala Phe Val Ser Gln				1828
585	590	595	600	
tct ttt tca tca cca gat ctt ttt gtt aaa caa act aga agt ggt ctc Ser Phe Ser Ser Pro Asp Leu Phe Val Lys Gln Thr Arg Ser Gly Leu				1876
605	610	615		
att tgg agt gat ctt gag ttt gat cca aca aca tct att tgg tat gtt Ile Trp Ser Asp Leu Glu Phe Asp Pro Thr Thr Ser Ile Trp Tyr Val				1924
620	625	630		
aat aat atc caa gca tct caa gat ttt tac tct ttc tct att gct cgt Asn Asn Ile Gln Ala Ser Gln Asp Phe Tyr Ser Phe Ser Ile Ala Arg				1972
635	640	645		
gag act act aac tgg cta aga caa caa cat ata tgg act cta caa aac Glu Thr Thr Asn Trp Leu Arg Gln Gln His Ile Trp Thr Leu Gln Asn				2020
650	655	660		
cgt tca agt aaa ctt tta gac aac gaa cat tat gga cta tgg ata aat Arg Ser Ser Lys Leu Leu Asp Asn Glu His Tyr Gly Leu Trp Ile Asn				2068
665	670	675	680	
gtt caa ggt gga cat gaa agt ctt gat act tct att ggt agc aaa gca Val Gln Gly Gly His Glu Ser Leu Asp Thr Ser Ile Gly Ser Lys Ala				2116
685	690	695		

aaa atg cca tgg ata atg gca aca gca gga tat gac tat ctt caa caa Lys Met Pro Trp Ile Met Ala Thr Ala Gly Tyr Asp Tyr Leu Gln Gln 700 705 710	2164
cta cca agg tta gat atg aaa gcc ctt tat ggt ctt gct ttt ggt gct Leu Pro Arg Leu Asp Met Lys Ala Leu Tyr Gly Leu Ala Phe Gly Ala 715 720 725	2212
tct aaa ggt aaa agt aaa tgg tct agc gtc aac tct aca aaa aat gat Ser Lys Gly Lys Ser Lys Trp Ser Ser Val Asn Ser Thr Lys Asn Asp 730 735 740	2260
gct gag cta ggt atg gtt agt ggt tat gta ggt ctt atc cat aac aaa Ala Glu Leu Gly Met Val Ser Gly Tyr Val Gly Leu Ile His Asn Lys 745 750 755 760	2308
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cat act aat tct aca ggg ttc tat aga aat ttt aaa tgg aca gaa aca His Thr Asn Ser Thr Gly Phe Tyr Arg Asn Phe Lys Trp Thr Glu Thr 780 785 790	2404
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ggt att aaa atg aat cct cgt gga caa ctt att ttt gaa caa aca tct Gly Ile Lys Met Asn Pro Arg Gly Gln Leu Ile Phe Glu Gln Thr Ser 810 815 820	2500
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cta cca gtt acc aca cct att aat ctt tat gct ggt att gaa agg ata Leu Pro Val Thr Thr Pro Ile Asn Leu Tyr Ala Gly Ile Glu Arg Ile 860 865 870	2644
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aca aat ata tta ttg gga gaa cat ttt aat att cac tgt gat ata ttt Thr Asn Ile Leu Leu Gly Glu His Phe Asn Ile His Cys Asp Ile Phe 905 910 915 920	2788
gga gat aaa gga aat Gat aaa ggc att ggt ggg caa gca gga ttt aca Gly Asp Lys Gly Asn Asp Lys Gly Ile Gly Gly Gln Ala Gly Phe Thr 925 930 935	2836
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Ala Ala Asp Val Phe Phe Glu Gly Arg Thr Glu Thr Leu Ile Asn Val
35 40 45

Asn Lys Pro Phe Asp Ser Phe Phe Gly Gly Ser Asp Ser Thr Ile Gly
50 55 60

Thr Leu Glu Thr Gly Pro Thr Asn Leu Thr Phe Thr Thr Val Gly Ala
65 70 75 80

Phe Arg Asn Ser Val Phe Arg Ile Ile Gly Gly Arg Ser Ser Phe
85 90 95

Asn Asn Pro Asn Thr Val Lys Gly Asn Val Thr Leu Thr Val Tyr Asn
100 105 110

Thr Asp Val Glu Arg Ile Ile Gly Ala Gly Ile Ser Asn Arg Gly Leu
115 120 125 .

Val Thr Val Thr Gly Ser Val Asn Met Lys Leu Glu Asn Val Ser Val
130 135 140

Thr Arg Gly Ile Tyr Gly Val Tyr Thr Gln Asn Gly His Val Leu
145 150 155 160

Gly Ser Ile Asn Met His Leu Lys Asn Val Gln Thr Pro Leu Leu Ile
165 170 175

Gly Ser Gly Val Ser Asn Gly Pro Asn Arg Ile Thr Val Asn Gly Asp
180 185 190

Ile Asn Ile Asp Val Glu Asp Ser Arg Ile Gln Tyr Val Asn Ile Thr
195 200 205

Gly Glu Val Asp Ala Gly Ile Lys Gly Asn Ala Thr Leu Thr Val Lys
210 215 220

Lys Ser Thr Val Glu Leu Ile Asn Ser Gly Arg Gly Asn Ile Leu Gly

225

230

235

240

Asn Leu Lys Ile Ser Ile Ala Asp Ser Asn Ile Arg Gly Leu Ser Pro
245 250 255

Val Asp Phe Gly Ser Ser Val Tyr Gly Asp Thr Ser Ile Asn Val Ile
260 265 270

Asn Ser Gln Ile Asn Asp Ile Thr Leu Ile Pro Arg Ala Gly Gly Met
275 280 285

Leu Val Gly Pro Val Thr Leu Asp Ile Thr Ser Ser Thr Ile Gln Asn
290 295 300

Ile Gln Cys Gly Pro Val Ser Gln Asn Asn Gln Leu Asn Thr Leu Asn
305 310 315 320

Val Thr Val Asn Thr Ser Asn Ile Thr Asn Leu Asn Leu Gly Ser Val
325 330 335

Glu Gly His Thr Ile Ser Thr Thr Ala Thr Val Thr Asp Ser Asn Ile
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Thr Asn Leu Asn Val Gly Thr Phe Asn Gly Leu Gly Val Thr Glu Asn
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Ala Ser Val Ile Ile Asn Ser Gly Asn Ile Thr Asn Leu Asn Val Gly
370 375 380

Thr Asn Val Ile Ala Ala Ala Thr Thr Ile Asn Ser Ser Ala Thr Ile
385 390 395 400

His Asp Gly Leu Ile Ala Asn Leu Thr Leu Gly Ser Gln Gly Asn Gly
405 410 415

Arg Thr Met Ile Ala Thr Ala Asn Val Asn Gly Gly Thr Ile Gly Leu
420 425 430

Leu Thr Met Gly Ser Glu Asn Phe Ile Pro Gly Thr Arg Pro Ile Thr
435 440 445

Glu Leu Ala Ile Leu Asn Met Ser Gly Gly Leu Ile Glu Arg Ile Ile
450 455 460

Val Gly Asn Ala Asn Ser Ser Thr Ile Asn Phe Thr Pro Gly Lys Arg
465 470 475 480

Ser Ile Val Lys Thr Ile Asn Gly Pro Glu Leu Pro Tyr Leu Val Asn
485 490 495

Ile Gln Lys Gly Ala Met Thr Gln Trp Gly Thr Lys Asn Met Pro Phe
500 505 510

Leu Leu Asp Thr Arg Asn Leu Ile Leu Ser Gly Thr Leu Ile Thr Ser
515 520 525

Asn Ile Gln Leu Ala Asp Leu Ser Ile Thr Asn Leu Phe Val Ala Asn
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Gly Gly Thr Leu Val Pro Arg Lys Leu Ile Pro Gly Asn Gln Pro Val
545 550 555 560

Ile Gln Phe Leu Gly Gly Pro Gln Ser Leu Leu Val Ile His Gln Pro
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Leu Lys Val Asn Leu Ser Leu Ser Pro Lys Leu Ile Gly Ser Ser Met
580 585 590

Val Pro Leu Ala Phe Val Ser Gln Ser Phe Ser Ser Pro Asp Leu Phe
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Val Lys Gln Thr Arg Ser Gly Leu Ile Trp Ser Asp Leu Glu Phe Asp
610 615 620

Pro Thr Thr Ser Ile Trp Tyr Val Asn Asn Ile Gln Ala Ser Gln Asp
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Phe Tyr Ser Phe Ser Ile Ala Arg Glu Thr Thr Asn Trp Leu Arg Gln
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Gln His Ile Trp Thr Leu Gln Asn Arg Ser Ser Lys Leu Leu Asp Asn
660 665 670

Glu His Tyr Gly Leu Trp Ile Asn Val Gln Gly Gly His Glu Ser Leu
675 680 685

Asp Thr Ser Ile Gly Ser Lys Ala Lys Met Pro Trp Ile Met Ala Thr
690 695 700

Ala Gly Tyr Asp Tyr Leu Gln Gln Leu Pro Arg Leu Asp Met Lys Ala
705 710 715 720

Leu Tyr Gly Leu Ala Phe Gly Ala Ser Lys Gly Lys Ser Lys Trp Ser
725 730 735

Ser Val Asn Ser Thr Lys Asn Asp Ala Glu Leu Gly Met Val Ser Gly
740 745 750

Tyr Val Gly Leu Ile His Asn Lys Thr Gly Leu Tyr Ser Thr Leu Thr
755 760 765

Leu Gln Leu Ala Ser Ser Lys Leu His Thr Asn Ser Thr Gly Phe Tyr
770 775 780

Arg Asn Phe Lys Trp Thr Glu Thr Thr Pro Thr Glu Ala Leu Glu Leu
785 790 795 800

Gly Trp Lys Tyr Thr Phe Asn Asn Gly Ile Lys Met Asn Pro Arg Gly
805 810 815

Gln Leu Ile Phe Glu Gln Thr Ser Lys His His Phe Asp Leu Gly Ile
820 825 830

Gln Asn Asp Lys Ala Ile Leu Asp Lys Ser Gln Leu Ile Thr Ser Ser
835 840 845

Leu Gly Ile Thr Val Glu Tyr Lys Leu Pro Val Thr Thr Pro Ile Asn
850 855 860

Leu Tyr Ala Gly Ile Glu Arg Ile Lys Gly Gln Ser Gly Asn Phe Ala
865 870 875 880

Ile Ser Ser Gln Ser Leu Gln Met Lys Phe Lys His Asp Asn Asp Thr
885 890 895

Ser Val Val Arg Ala Thr Ile Gly Thr Asn Ile Leu Leu Gly Glu His
900 905 910

Phe Asn Ile His Cys Asp Ile Phe Gly Asp Lys Gly Asn Asp Lys Gly
915 920 925

Ile Gly Gly Gln Ala Gly Phe Thr Tyr Lys Phe
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